a.) Amendment to the Claims

1. (Currently Amended) A process for producing an amino acid, which comprises the steps of:

culturing, in a medium, a microorganism expressing a heterologous DNA encoding a NADH dehydrogenase in which the number of protons discharged per electron is zero, said heterologous DNA being ~~selected from the group consisting of (i) SEQ ID NOS: 3, 5, 7, 9, 11, 13 and 15, and~~ (i) SEQ ID NO:3 or (ii) a DNA which hybridizes, under stringent conditions, with a DNA having a nucleotide sequence complementary to the full-length nucleotide sequence of ~~a DNA selected from the group consisting of SEQ ID NOS:3, 5, 7, 9, 11, 13 and 15~~ SEQ ID NO:3,

forming and accumulating an amino acid in a culture, and

recovering the amino acid from the culture,

wherein said stringent condition comprise hybridization at 65°C in the presence of 0.7 to 1.0 mol/l NaCl on a filter having fixed DNA followed by washing at 65°C using 0.1 to 2-fold SSC.

2. (Currently Amended) The process according to claim 1, wherein the heterologous DNA of ~~encoding NADH dehydrogenase~~ (i) or (ii) is derived from a microorganism selected from the group consisting of *Corynebacterium, Escherichia, Pseudomonas, Azotobacter, Salmonella* and *Lactobacillus*.

3. (Currently Amended) The process according to claim 2, wherein the heterologous DNA of ~~encoding NADH dehydrogenase~~ (i) or (ii) is derived from a microorganism selected from the group consisting of *Corynebacterium glutamicum, Corynebacterium diphtheriae, Escherichia coli, Pseudomonas fluorescens, Azotobacter vinelandii, Salmonella typhimurium* and *Lactobacillus plantarum.*

Claim 4 (Cancelled).

5. (Currently Amended) The process according to claim 1, wherein the heterologous DNA of ~~encoding NADH dehydrogenase~~ (i) or (ii) is DNA within the plasmid pCS-CGndh within *Escherichia coli* DH5α/pCS-CGndh.

6. (Currently Amended) The process according to claim 1, wherein the NADH dehydrogenase is a polypeptide comprising (1) SEQ ID NO:4 or (2) SEQ ID NO:4 ~~having an amino acid sequence selected from the group consisting SEQ ID NOs: 4, 6, 8, 10, 12, 14 and 16, and a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS:4, 6, 8, 10, 12, 14 and 16~~ wherein 1 to 20 amino acid residues are deleted, substituted or added in the amino acid sequence of the polypeptide.

Claim 7 (Cancelled).

8. (Previously Presented) The process according to claim 1, wherein the microorganism is selected from the group consisting of *Escherichia, Corynebacterium, Brevibacterium, Arthrobacter, Aureobacterium, Cellulomonas, Clavibacter, Curtobacterium, Microbacterium, Pimerobacter* and *Bacillus.*

9. (Previously Presented) The process according to claim 1, wherein the microorganism belongs to the genus *Escherichia.*

10. (Previously Presented) The process according to claim 1, wherein the microorganism belongs to the species *Escherichia coli.*

11. (Previously Presented) The process according to claim 1, wherein the microorganism belongs to the genus *Corynebacterium.*

12. (Previously Presented) The process according to claim 1, wherein the microorganism is selected from the group consisting of *Corynebacterium glutamicum,*

Corynebacterium flavum, Corynebacterium lactofermentum, and *Corynebacterium efficasis*.

13. (Previously Presented) The process according to claim 1, wherein the microorganism belongs to the species *Corynebacterium glutamicum*.

14. (Previously Presented) The process according to claim 1, wherein the amino acid is selected from the group consisting of L-glutamic acid, L-glutamine, L-aspartic acid, L-asparagine, L-lysine, L-methionine, L-threonine, L-arginine, L-proline, L-citrulline, L-valine, L-leucine, L-isoleucine, L-serine, L-cysteine, glycine, L-tryptophan, L-tyrosine, L-phenylalanine and L-histidine.

15. (Previously Presented) The process according to claim 1, wherein the amino acid is selected from the group consisting of L-glutamic acid, L-glutamine and L-lysine.

Claims 16-26 (Cancelled).